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<!--StartFragment-->RESULT 6
US-10-199-937-135
; Sequence 135, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-135

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Query Match          99.9%; Score 5582; DB 4; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSEFGHAEVVNLLLRHGADPNARDNWNYYT 60
        |||
Db      67 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSEFGHAEVVNLLLRHGADPNARDNWNYYT 126
        |||

Qy      61 PLHEAAIKGKIDVCIVLLQHGAETIRNTDGR TALDLADPSAKAVLTGEYKKDELLESAR 120
        |||
Db      127 PLHEAAIKGKIDVCIVLLQHGAETIRNTDGR TALDLADPSAKAVLTGEYKKDELLESAR 186
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Qy      121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180
        |||
Db      187 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 246
        |||

Qy      181 PLHNACSYGHYEVTLLVKHGACVNAMD LWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
        |||
Db      247 PLHNACSYGHYEVTLLVKHGACVNAMD LWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 306
        |||

Qy      241 NCHNKSAIDLAPTPQLKERLAYEFKGHSL LQAAREADVTRIKKHL SLEMVNFKHPQTHET 300
        |||
Db      307 NCHNKSAIDLAPTPQLKERLAYEFKGHSL LQAAREADVTRIKKHL SLEMVNFKHPQTHET 366
        |||

Qy      301 ALHCAAASPYPKRKQICELLRLRGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360
        |||
Db      367 ALHCAAASPYPKRKQICELLRLRGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 426
        |||

Qy      361 NALDNLGQTS LHRAAYCGHLQTCRLLLSYGCDPNII SLQGFTALQMGNE NVQQLQEGIS 420
        |||
Db      427 NALDNLGQTS LHRAAYCGHLQTCRLLLSYGCDPNII SLQGFTALQMGNE NVQQLQEGIS 486
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Qy      421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
        |||
Db      487 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546
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Qy	481	QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE	540
Db	547	QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE	606
Qy	541	ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS	600
Db	607	ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS	666
Qy	601	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660
Db	667	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	726
Qy	661	VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLAHGADPTLKNQEGQTPDLVLS	720
Db	727	VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLAHGADPTLKNQEGQTPDLVLS	786
Qy	721	ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG	780
Db	787	ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG	846
Qy	781	SFSELSSVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE	840
Db	847	SFSELSSVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE	906
Qy	841	MGHKELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ	900
Db	907	MGHKELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ	966
Qy	901	SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLWERYTHRRKEVSEENHNHANE	960
Db	967	SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLWERYTHRRKEVSEENHNHANE	1026
Qy	961	RMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD	1020
Db	1027	RMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD	1086
Qy	1021	RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV	1065
Db	1087	RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV	1131

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Qy	507	EVAELLVKHGAVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLV	566
Db	481	EVAELLVKHGAVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLV	540
Qy	567	KDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNL	626
Db	541	KDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNL	600
Qy	627	EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEA	686
Db	601	EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNASLNATDKWAFTPLHEA	660
Qy	687	AQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVL	746
Db	661	AQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVL	720
Qy	747	NGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVSSSGTEGASSLEKKEVP	806
Db	721	NGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVSSSGTEGASSLEKKEVP	780
Qy	807	GVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKVER	866
Db	781	GVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKVER	840
Qy	867	LISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRY	926
Db	841	LISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRY	900
Qy	927	NILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIHKGFDERHAYIG	986
Db	901	NILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIHKGFDERHAYIG	960
Qy	987	GMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSA	1046
Db	961	GMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSA	1020
Qy	1047	MKMAHSPPGHHSVTGRPSV	1065
Db	1021	MKMAHSPPGHHSVTGRPSV	1039

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